

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:11 ; Search time 47.2765 Seconds
(without alignments)
1199.218 Million cell updates/sec

Title: US-10-724-274-1
Perfect score: 657
Sequence: 1 QVQLKSGGLVAPSSQSLT.....TTGDDALDYGQTSVTVSS 124

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*
10: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	657	100.0	124	8	Adt77619 IIA1 VH p
2	657	100.0	124	9	Aeb51138 Mouse ant
3	657	100.0	143	8	Adq31879 Antibody
4	657	100.0	143	8	Adq31905 Murine an
5	657	100.0	143	8	Adq31875 Antibody
6	657	100.0	143	8	Adt77638 Antibody
7	657	100.0	143	8	Adt77634 Antibody
8	657	100.0	143	9	Aeb51153 Chimeric
9	657	100.0	143	9	Aeb51180 Chimeric
10	657	100.0	143	9	Aed49294 Anti-alpha
11	657	100.0	143	9	Aed49290 Anti-alpha
12	657	100.0	232	8	Adq31887 Antibody
13	657	100.0	232	8	Adt77646 Chimeric
14	657	100.0	232	9	Aeb51165 Chimeric
15	657	100.0	451	8	Adq31884 Antibody
16	657	100.0	451	8	Adt51712 M200 anti
17	657	100.0	451	8	Adt51711 M200 anti
18	657	100.0	451	8	Adt51709 M200 anti
19	657	100.0	451	8	Adt51713 M200 anti
20	657	100.0	451	8	Adt51710 M200 anti
21	657	100.0	451	8	Adt77643 Antibody
22	657	100.0	451	9	Aeb51162 Chimeric
23	657	100.0	451	10	Aef12090 Anti-alpha

24	657	100.0	451	10	Aef16428	Chimeric
25	657	100.0	451	10	Aef16425	Chimeric
26	657	100.0	451	10	Aef16426	Chimeric
27	657	100.0	451	10	Aef16427	Chimeric
28	657	100.0	451	10	Aef16424	Chimeric
29	627	95.4	136	9	Aeb51157	Chimeric
30	568	86.5	124	8	Adq31861	Humanized
31	568	86.5	124	8	Adt77620	1 VH pept
32	568	86.5	124	9	Aeb51139	Humanized
33	559	85.1	124	8	Adq31865	Humanized
34	559	85.1	124	8	Adt77624	5 VH pept
35	550	85.1	124	9	Aeb51143	Humanized
36	550	83.7	124	8	Adq31864	Humanized
37	550	83.7	124	8	Adt77623	4 VH pept
38	550	83.7	124	9	Aeb51142	Humanized
39	549	83.6	124	8	Adq31862	Humanized
40	549	83.6	124	8	Adt77621	2 VH pept
41	549	83.6	124	9	Aeb51140	Humanized
42	539	82.0	451	8	Adq31890	Antibody
43	539	82.0	451	9	Aeb51168	Chimeric
44	536.5	81.7	119	10	Aef10439	Mouse mab
45	522	79.5	124	8	Adq31863	Humanized

ALIGNMENTS

RESULT 1
ADT77619
ID ADT77619 standard; peptide; 124 AA.

XX AC ADT77619;

XX DT 13-JAN-2005 (first entry)

XX DE IIA1 VH peptide.

XX heavy; chain; variable; region; light; constant; antibody;
XX macrophage behaviour; wound site; eye; alphasbetal;
XX integral binding agent; RPS cell; phagocytic activity; secretion;
XX cytokine; chemokine; mediator; ligament; tendon; keloid formation; burn;
XX bone; cartilage; vascular; ligament; inflammatory response; granulation;
XX scleroderma; tissue inflammation; rheumatoid arthritis;
XX Wegener's Granulomatosis; Churg-Strauss-allergic granulomatosis;
XX eosinophilic granulomata; midline granuloma; demoid; sarcoidosis;
XX macular degeneration; proliferative vitreoretinopathy;
XX proliferative diabetic retinopathy; uterine fibroid;
XX arteritis temporalis; Takayasu's arteritis; Crohn's disease;
XX idiopathic pulmonary fibrosis; allergic pulmonary fibrosis;
XX wound healing; scar formation.

XX OS Homo sapiens.

Key	Location/Qualifiers
Peptide	1..25 /label= FR1
Peptide	4..124 /label= FR4
Peptide	26..35 /label= CDR1
Peptide	36..49 /label= FR2
Peptide	50..65 /label= CDR2
Peptide	66..97 /label= FR3
Peptide	98..113 /label= CDR3

XX W02004089988-A2.

XX 21-OCT-2004.

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:59:30 ; Search time 13.0696 Seconds
(without alignments)
830.460 Million cell updates/sec

Title: US-10-724-274-1

Perfect score: 657

Sequence: 1 QVQLKESGRLVAPSSQSLSI.....TTTGDALDYWGQGTSTVTVSS 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SID3S/ptodata/2/iaa/5 COMB.pcp.*
- 2: /EMC_Celerra_SID3S/ptodata/2/iaa/6 COMB.pcp.*
- 3: /EMC_Celerra_SID3S/ptodata/2/iaa/7 COMB.pcp.*
- 4: /EMC_Celerra_SID3S/ptodata/2/iaa/H COMB.pcp.*
- 5: /EMC_Celerra_SID3S/ptodata/2/iaa/PCTUS COMB.pcp.*
- 6: /EMC_Celerra_SID3S/ptodata/2/iaa/RE COMB.pcp.*
- 7: /EMC_Celerra_SID3S/ptodata/2/iaa/backfilese1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517.5	78.8	119	1	US-08-752-844-16
2	517.5	78.8	119	1	US-08-591-196-16
3	517.5	78.8	119	2	US-09-293-533-16
4	502	76.4	120	1	US-08-652-558-38
5	501.5	76.3	142	3	US-08-772-103-4
6	497	75.6	121	2	US-08-881-037-67
7	495.5	75.4	113	2	US-08-726-219A-218
8	495.5	75.4	113	2	US-08-196-522-218
9	492	74.9	140	2	US-08-943-136-4
10	492	74.9	140	2	US-08-973-518-4
11	490	74.6	116	2	US-09-232-290-36
12	490	74.6	135	2	US-10-351-748-31
13	489	74.4	239	1	US-08-860-174A-2
14	489	74.4	241	2	US-08-726-219A-187
15	489	74.4	241	2	US-09-196-522-187
16	489	74.4	272	2	US-09-726-219A-183
17	489	74.4	272	2	US-09-196-522-183
18	487.5	74.2	121	2	US-10-056-052A-12
19	486	74.0	116	2	US-10-194-975-100
20	486	74.0	137	1	US-08-621-751A-4
21	485.5	73.9	222	1	US-08-190-199A-67
22	485.5	73.9	222	1	US-08-190-199A-61
23	483.5	73.6	119	2	US-08-483-749A-14
24	481	73.2	112	2	US-09-189-129-3
25	481	73.2	112	2	US-09-824-286-3
26	479.5	73.0	152	1	US-08-752-844-16

27 479.5 73.0 152 1 US-08-591-196-4 Sequence 4, Appli
28 479.5 73.0 152 2 US-09-192-838B-4 Sequence 4, Appli
29 479.5 73.0 152 2 US-09-293-533-4 Sequence 4, Appli
30 479.5 73.0 152 2 US-09-324-191-4 Sequence 4, Appli
31 479.5 73.0 263 1 US-08-752-844-66 Sequence 66, Appli
32 479.5 73.0 263 2 US-09-293-533-66 Sequence 15, Appli
33 479.5 72.8 119 1 US-08-667-769A-15 Sequence 15, Appli
34 479.5 72.8 119 2 US-10-700-740-15 Sequence 15, Appli
35 478.5 72.8 242 7 5455030-15 Patent No. 5455030
36 478.5 72.8 242 7 5455030-15 Patent No. 5455030
37 477.5 72.7 115 2 US-10-056-052A-24 Sequence 24, Appli
38 477 72.6 241 2 US-09-554-765-13 Sequence 13, Appli
39 474 72.1 118 2 US-10-056-052A-16 Sequence 16, Appli
40 468 71.2 116 2 US-08-397-411-4 Sequence 4, Appli
41 468 71.2 122 2 US-09-232-290-41 Sequence 41, Appli
42 467 71.1 120 2 US-10-194-975-112 Sequence 112, App
43 466.5 71.0 107 1 US-08-122-546-12 Sequence 12, Appli
44 466.5 71.0 107 1 US-08-764-938-12 Sequence 12, Appli
45 466.5 71.0 107 2 US-09-131-052-12 Sequence 12, Appli

ALIGNMENTS

RESULT 1

US-08-752-844-16
; Sequence 16, Application US/08752844
; Patent No. 5935821

; GENERAL INFORMATION:

; APPLICANT: Chatterjee, Malaya

; APPLICANT: Poon, Kenneth A.

; APPLICANT: Chatterjee, Sunil K.

; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 PAGE MILL ROAD

; CITY: PALO ALTO

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/752,844

; FILING DATE:

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Schiff, J. Michael

; REGISTRATION NUMBER: 40,253

; REFERENCE/DOCKET NUMBER: 30414-20002.21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 813-5600

; TELEFAX: (415) 494-0792

; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-752-844-16

Query Match 78.8%; Score 517.5; DB 1; Length 119;

Best Local Similarity 80.2%; Pred. No. 8.7e-42;

Matches 101; Conservative 6; Mismatches 10; Indels 9; Gaps 2;

Qy

1 QVQLKESGRLVAPSSQSLSICTISGFLTDYGVHWRQPPGKGLVWLVIWSDGSSTYN 60

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:47:35 ; Search time 7.42225 Seconds

(without alignments)
1607.447 Million cell updates/sec

Title: US-10-724-274-1

Perfect score: 657

Sequence: 1 QVQLKESGPGLVAPQSLSLSTCTISGFSLTSGVHVVQPPGKGLVWLVSDGSTYN 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.* ;

1: pir1.* ;

2: pir2.* ;

3: pir3.* ;

4: pir4.* ;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	510	77.6	144	2	S11244	Ig gamma-2a chain
2	503	76.6	122	2	S20809	Ig heavy chain v r
3	500.5	76.2	144	1	G2MS14	Ig heavy chain pre
4	499	76.0	117	2	S38563	Ig heavy chain v r
5	492	74.9	141	2	S52446	Ig heavy chain v r
6	490	74.6	120	2	PL0087	Ig heavy chain v r
7	489	74.4	122	2	A49049	Ig heavy chain v r
8	488.5	74.4	140	2	S55028	Ig heavy chain v r
9	484.5	73.7	114	2	S11106	Ig heavy chain v r
10	478.5	72.8	112	2	S11100	Ig heavy chain v r
11	475.5	72.4	111	2	S26324	Ig heavy chain v r
12	473	72.0	139	2	A32456	Ig heavy chain pre
13	472.5	71.9	231	2	PC4155	Ig gamma-2b chain
14	470	71.5	118	2	S32786	Ig heavy chain (an
15	469.5	71.5	112	2	S11108	Ig heavy chain v r
16	469.5	71.5	116	2	S11102	Ig heavy chain v r
17	469.5	71.5	140	2	S14238	Ig gamma-1 chain p
18	469	71.4	116	2	S42484	Ig heavy chain v r
19	468.5	71.3	110	2	S26323	Ig heavy chain v r
20	467.5	71.2	113	2	S11101	Ig heavy chain v r
21	466	70.9	101	2	S03466	Ig heavy chain v r
22	466	70.9	135	2	S31913	Ig gamma-2a chain
23	465.5	70.9	118	2	PQ0266	Ig heavy chain v r
24	463.5	70.5	114	2	S11099	Ig heavy chain v r
25	463.5	70.5	127	2	B31807	Ig heavy chain v r
26	458.5	69.8	115	2	S11103	Ig heavy chain v r
27	457.5	69.6	106	2	S26322	Ig heavy chain v r
28	454.5	69.2	106	2	S14489	Ig heavy chain v r
29	452.5	68.9	121	2	D30560	Ig heavy chain v r

ALIGNMENTS

RESULT 1

S11244

Ig gamma-2a chain precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

C:Accession: S11244

R:Wellman, A.A.; Meares, C.F., 1990

Nucleic Acids Res. 18, 5281, 1990

A:Title: Sequences of the T_H1 antibody heavy and light chain variable regions.

A:Reference number: S11244; MUID:90384832; PMID:2119497

A:Accession: S11244

A:Molecule type: mRNA

A:Residues: 1-144 <WEL>

A:Cross-references: UNIPARC:UPI0000176C81; EMBL:X53483

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

P:34-116/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 510; DB 2; Length 144;

Best Local Similarity 81.5%; Pred. No. 1.6e-38;

Matches 101; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

Oy 1 QVQLKESGPGLVAPQSLSLSTCTISGFSLTSGVHVVQPPGKGLVWLVSDGSTYN 60

Db 20 QVQLKESGPGLVAPQSLSLSTCTISGFSLTSGVHVVQPPGKGLVWLVSDGSTYN 79

Oy 61 SALKSRMTIRKDNKSKSQVFLIMNSLQTDSDSAMYTCARHGTYYGTTTGDALDYWGQGTSV 120

Db 80 SALKSRMTIRKDNKSKSQVFLIMNSLQTDSDSAMYTCARHGTYYGTTTGDALDYWGQGTSV 133

Oy 121 TVSS 124

Db 134 TVSA 137

RESULT 2

S20809

Ig heavy chain V region (hybridoma C8) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S20809

R:Hoogenboom, H.; Dubois, P.; Raus, J.; Volckaert, G.

submitted to the EMBL Data Library, September 1990

A:Description: Nucleotide sequences of the variable region cDNAs encoding a murine ant

A:Reference number: S20809

A:Accession: S20809

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-122 <HOOG>

A:Cross-references: UNIPARC:UPI000011588E; EMBL:X54692; NID:G50249; PIDN:CAA38508.1; F

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	500.5	76.2	144	1	HV43_MOUSE	P01819 mus musculus
2	499	76.0	484	2	Q50472_MOUSE	Q50472 mus musculus
3	483	73.5	482	2	Q91X92_MOUSE	Q91X92 mus musculus
4	481	73.2	121	2	Q99NG4_MOUSE	Q99NG4 mus musculus
5	470	71.5	591	2	Q51019_RAT	Q51019 rattus norv
6	456.5	69.5	469	2	Q5M839_RAT	Q5M839 rattus norv
7	444.5	67.7	477	2	Q510J1_RAT	Q510J1 rattus norv
8	435.5	66.3	458	2	Q5M842_RAT	Q5M842 rattus norv
9	435	66.2	115	1	HV44_MOUSE	P01820 mus musculus
10	406	61.8	116	1	HV45_MOUSE	P01821 mus musculus
11	379	57.7	485	2	Q561M5_MOUSE	Q561M5 mus musculus
12	376.5	57.3	487	2	Q58E53_MOUSE	Q58E53 mus musculus
13	373	56.8	135	1	HV02_XENLA	P20957 xenopus lae
14	373	56.8	483	2	Q5UA13_MOUSE	Q5UA13 mus musculus
15	367	55.9	550	2	Q4V801_XENLA	Q4V801 xenopus lae
16	367	55.9	573	2	Q8W038_HUMAN	Q8W038 homo sapien
17	364.5	55.5	485	2	Q58B54_MOUSE	Q58B54 mus musculus
18	363	55.3	617	2	Q569B3_RAT	Q569B3 rattus norv
19	357.5	54.4	476	2	Q6GMX1_HUMAN	Q6GMX1 homo sapien
20	354.5	54.0	119	2	Q9UL73_HUMAN	Q9UL73 homo sapien
21	352.5	53.7	121	1	HV3J_HUMAN	P01771 homo sapien
22	351	53.4	477	2	Q6GMX7_HUMAN	Q6GMX7 homo sapien
23	350.5	53.3	240	2	Q65ZC9_HUMAN	Q65ZC9 homo sapien
24	350	53.3	118	2	Q81IU5_MOUSE	Q81IU5 mus musculus
25	350	53.3	478	2	Q5FVQ3_RAT	Q5FVQ3 rattus norv
26	349.5	53.2	472	2	Q6N089_HUMAN	Q6N089 homo sapien
27	349	53.1	465	2	Q6GMX6_HUMAN	Q6GMX6 homo sapien
28	349	53.1	469	2	Q569F4_HUMAN	Q569F4 homo sapien
29	346	52.7	126	1	HV3K_HUMAN	P01772 homo sapien
30	345.5	52.6	136	1	HV01_XENLA	P20956 xenopus lae
31	345.5	52.6	615	2	Q569B6_RAT	Q569B6 rattus norv

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:11 ; Search time 54.5205 Seconds
(without alignments)
1199.218 Million cell updates/sec

Title: US-10-724-274-16
Perfect score: 752
Sequence: 1 MAVGLLLCLVTFPSCVLSQ.....TTTGDAIDYWGQGTSTVSS 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.8.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*
- 10: Geneseq2006s.*

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	752	100.0	143	8 ADQ31879	Adq31879 Antibody
2	752	100.0	143	8 ADQ31905	Adq31905 Murine an
3	752	100.0	143	8 ADQ31875	Adq31875 Antibody
4	752	100.0	143	8 ADT77638	Adt77638 Antibody
5	752	100.0	143	8 ADT77634	Adt77634 Antibody
6	752	100.0	143	9 AEB51153	Aeb51153 Chimeric
7	752	100.0	143	9 AEB51180	Aeb51180 Chimeric
8	752	100.0	143	9 AED49294	Aed49294 Anti-alph
9	752	100.0	143	9 AED49290	Aed49290 Anti-alph
10	722	96.0	136	9 AEB51157	Aeb51157 Chimeric
11	657	87.4	124	9 AEB51157	Adt77619 IIAL VH p
12	657	87.4	124	9 AEB51138	Aeb51138 Mouse ant
13	657	87.4	232	8 ADQ31887	Adt77646 Antibody
14	657	87.4	232	8 ADQ31884	Aeb51165 Chimeric
15	657	87.4	232	9 AEB51165	Adq31884 Antibody
16	657	87.4	451	8 ADQ31884	Adt51712 M200 anti
17	657	87.4	451	8 ADT51712	Adt51711 M200 anti
18	657	87.4	451	8 ADT51711	Adt51709 M200 anti
19	657	87.4	451	8 ADT51709	Adt51713 M200 anti
20	657	87.4	451	8 ADT51713	Adt51710 M200 anti
21	657	87.4	451	8 ADT51710	Adt77643 Antibody
22	657	87.4	451	8 ADT77643	Aeb51162 Chimeric
23	657	87.4	451	9 AEB51162	

24	657	87.4	451	10 AEF12090	Aef12090 Anti-alph
25	657	87.4	451	10 AEF16428	Aef16428 Chimeric
26	657	87.4	451	10 AEF16425	Aef16425 Chimeric
27	657	87.4	451	10 AEF16426	Aef16426 Chimeric
28	657	87.4	451	10 AEF16427	Aef16427 Chimeric
29	657	87.4	451	10 AEF16424	Aef16424 Chimeric
30	581.5	77.3	183	2 AAR15326	Aar15326 IL-2 chim
31	581.5	77.3	183	2 AAR32128	Aar32128 Anti-IL2R
32	580.5	77.2	138	2 RAW01146	Raw01146 MAb 10.1
33	575.5	76.5	358	5 AAE27929	Aae27929 Human CH2
34	575.5	76.5	358	5 ABB82838	Abb82838 Antibody
35	575.5	76.5	468	5 AAE27928	Aae27928 Human CSE
36	575.5	76.5	468	6 ABB82837	Abb82837 Antibody
37	574	76.3	135	1 AAP70991	Aap70991 Sequence
38	572.5	76.1	142	4 AAG66520	Aag66520 Mouse ant
39	571	75.9	137	2 AAW30277	Aaw30277 Heavy cha
40	570.5	75.9	152	2 AAY49210	Aay49210 MAB 1A7 h
41	570.5	75.9	152	2 AAY28469	Aay28469 Heavy cha
42	570.5	75.9	152	2 AAY21546	Aay21546 Monoclonal
43	570.5	75.9	152	6 ADA14770	Ada14770 Mouse ant
44	570.5	75.9	152	7 ADC35312	Adc35312 Monoclonal
45	570.5	75.9	152	10 AEF10365	Aef10365 Mouse mab

ALIGNMENTS

RESULT 1

ADQ31879 standard; protein; 143 AA.

ADQ31879; (first entry)
23-SEP-2004 (first entry)
Antibody M200 VH amino acid sequence SEQ ID NO:20.

chimeric anti-alpha5beta-1 integrin antibody; antibody; immunoreactive;
alpha5beta1 integrin; humanised anti-alpha5beta1 integrin antibody;
vascularisation; antiangiogenic; integrin alpha5beta5 antagonist.

Mus sp.

Homo sapiens.

Synthetic.

WO2004056308-A2.

08-JUL-2004.

26-NOV-2003; 2003WO-US038172.

26-NOV-2002; 2002US-0429743P.

(PROT-) PROTEIN DESIGN LABS INC.

Ramakrishnan V, Powers D, Johnson DE, Jeffrey U;

WPI; 2004-525316/50.

N-P8DB; ADQ31878.

New chimeric anti-alpha-5 beta-1 integrin antibody useful for controlling
vascularization in injured tissue.

Claim 23, SEQ ID NO 20; 89pp; English.

The present invention describes a chimeric anti-alpha5beta-1 integrin
antibody (I), comprising: (a) a first polypeptide sequence from a first
source comprising one or more amino acid sequences selected from SEQ ID
NOS: 1, 7, 16, 18, 20, 22, 25, 26, 28, 31 and 32; and (b) a second
polypeptide from a second source comprising a constant region sequence of
an antibody of the second source, where the first and second polypeptide
sequences form a protein complex, that is immunoreactive with alpha5beta1
integrin. Also described: (1) purifying (M1) pH-sensitive (I) comprises

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:59:30 ; Search time 15.0722 Seconds
(without alignments)
830.460 Million cell updates/sec

Title: US-10-724-274-16

Perfect score: 752

Sequence: 1 MAVLGILLCLVTPFPSCVLSQ.....TTTGDAIDYWGQTSVTSS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC Celerra SIDS3/ptodata/2/iaa/5_COMB.pdp:*
- 2: /EMC Celerra SIDS3/ptodata/2/iaa/6_COMB.pdp:*
- 3: /EMC Celerra SIDS3/ptodata/2/iaa/7_COMB.pdp:*
- 4: /EMC Celerra SIDS3/ptodata/2/iaa/8_COMB.pdp:*
- 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCBUS_COMB.pdp:*
- 6: /EMC Celerra SIDS3/ptodata/2/iaa/RB_COMB.pdp:*
- 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	574	76.3	135	2	US-10-351-748-31
2	572.5	76.1	142	3	US-09-772-103-4
3	571	75.9	137	1	US-08-621-751A-4
4	570.5	75.9	152	1	US-08-752-844-4
5	570.5	75.9	152	1	US-08-591-196-4
6	570.5	75.9	152	2	US-09-192-838B-4
7	570.5	75.9	152	2	US-09-293-533-4
8	570.5	75.9	152	2	US-09-324-191-4
9	570.5	75.9	263	1	US-08-752-844-66
10	570.5	75.9	263	2	US-09-293-533-66
11	552.5	73.5	478	2	US-09-770-916-2
12	542.5	72.1	138	1	US-07-634-278-33
13	542.5	72.1	138	1	US-08-477-728-33
14	542.5	72.1	138	1	US-08-474-040-33
15	542.5	72.1	138	1	US-08-487-200-33
16	542.5	72.1	138	2	US-08-484-537-33
17	542.5	72.1	138	3	US-09-718-998-33
18	541.5	72.0	140	2	US-08-943-136-4
19	541.5	72.0	140	2	US-08-973-518-4
20	522.5	69.5	142	3	US-09-772-103-10
21	517.5	68.8	119	1	US-08-752-844-16
22	517.5	68.8	119	1	US-08-591-196-16
23	517.5	68.8	119	2	US-09-293-533-16
24	517	68.8	137	1	US-08-621-751A-8
25	502	66.8	120	1	US-08-652-558-38
26	500.5	66.6	241	2	US-09-726-219A-187

27 500.5 66.6 241 2 US-09-196-522-187 Sequence 187, App
28 500.5 66.6 272 2 US-09-726-219A-183 Sequence 183, App
29 500.5 66.6 272 2 US-09-196-522-183 Sequence 183, App
30 497 66.1 121 2 US-08-881-037-67 Sequence 67, Appl
31 495.5 65.9 113 2 US-09-726-219A-218 Sequence 218, App
32 495.5 65.9 113 2 US-09-196-522-218 Sequence 218, App
33 493 65.6 239 1 US-08-860-174A-2 Sequence 2, Appl
34 490 65.2 116 2 US-09-232-290-36 Sequence 36, Appl
35 487.5 64.8 121 2 US-10-056-052A-12 Sequence 12, Appl
36 486 64.6 116 2 US-10-194-975-100 Sequence 100, App
37 485.5 64.6 222 1 US-08-190-199A-67 Sequence 67, Appl
38 485.5 64.6 235 1 US-08-190-199A-61 Sequence 14, Appl
39 483.5 64.3 119 2 US-08-483-749A-14 Sequence 61, Appl
40 481 64.0 112 2 US-09-189-129-3 Sequence 3, Appl
41 481 64.0 112 2 US-09-824-286-3 Sequence 13, Appl
42 481 64.0 241 2 US-09-554-765-13 Sequence 15, Appl
43 478.5 63.6 119 1 US-08-667-769A-15 Sequence 15, Appl
44 478.5 63.6 119 2 US-10-700-740-15 Sequence 15, Appl
45 478.5 63.6 119 5 PCT-US95-17082A-15

ALIGNMENTS

RESULT 1

US-10-351-748-31
; Sequence 31, Application US/10351748
; Patent No. 6982321
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; TITLE OF INVENTION: IMPROVEMENT IN OR RELATING TO ALTERED
; FILE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 7806-011-999 (CAM 107814-999010)
; CURRENT APPLICATION NUMBER: US/10/351,748
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 08/452,462
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 07/942,146
; PRIOR FILING DATE: 1992-09-08
; PRIOR APPLICATION NUMBER: 07/624,515
; PRIOR FILING DATE: 1990-12-07
; PRIOR APPLICATION NUMBER: 07/189,814
; PRIOR FILING DATE: 1988-05-03
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the variable domain gene of
; OTHER INFORMATION: antibody D1.3 (Fig 7)
US-10-351-748-31

Query Match 76.3%; Score 574; DB 2; Length 135;
Best Local Similarity 76.9%; Pred. No. 1.2e-48;
Matches 110; Conservative 11; Mismatches 14; Indels 8; Gaps 1;
QY 1 MAVLGILLCLVTPFPSCVLSQVLKESGPGGLVAPQSLSITCTISGSLTDYGVHWRQPP 60
Db 1 MAVLALLCLVTPFPSCILSQVLKESGPGGLVAPQSLSITCTISGSLTDYGVHWRQPP 60
QY 61 GKGLWLVWISDGSSTYNSALKSRMTIRKNSKSOVLIMNSLOTTDDSSAMYCYCARIGTY 120
Db 61 GKGLWLVWISDGSSTYNSALKSRMTIRKNSKSOVLIMNSLOTTDDSSAMYCYCARIGTY 120
QY 121 YGTTTGDALDYWGQTSVTSS 143
Db 121 -----RLDYWGQTSVTSS 135

RESULT 2

US-09-772-103-4

Result No.	Score	Query Match	Length	DB	ID	Description
1	605	80.5	144	2	S11244	Ig gamma-2a chain
2	580.5	77.2	141	1	D2MS14	Ig heavy chain pre
3	569	75.7	141	2	S52446	Ig heavy chain v r
4	565.5	75.2	140	2	S55028	Ig heavy chain v r
5	557	74.1	135	2	S33913	Ig gamma-2A chain
6	550	73.1	139	2	A32456	Ig heavy chain pre
7	529.5	70.4	140	2	S14238	Ig gamma-1 chain p
8	523	69.5	117	2	S10111	Ig heavy chain v r
9	519	69.0	115	1	HVMS14	Ig heavy chain pre
10	503	66.9	122	2	S20809	Ig heavy chain v r
11	499	66.4	117	2	S38563	Ig heavy chain v r
12	497	66.1	116	1	GLMS10	Ig heavy chain pre
13	496	66.0	116	2	A33932	Ig mu chain precu
14	490	65.2	120	2	PL0087	Ig heavy chain v r
15	489	65.0	122	2	AF9049	Ig heavy chain v r
16	484.5	64.4	114	2	S11106	Ig heavy chain v r
17	478.5	63.6	112	2	S11100	Ig heavy chain v r
18	477	63.4	101	2	S03466	Ig heavy chain v r
19	475.5	63.2	111	2	S26324	Ig heavy chain v r
20	472.5	62.8	231	2	PC4155	Ig gamma-2b chain
21	470	62.5	118	2	S32786	Ig heavy chain (an
22	469.5	62.4	112	2	S11108	Ig heavy chain v r
23	469.5	62.4	116	2	S11102	Ig heavy chain v r
24	469	62.4	116	2	S42484	Ig heavy chain v r
25	468.5	62.3	110	2	S26323	Ig heavy chain v r
26	467.5	62.2	113	2	S11101	Ig heavy chain v r
27	465.5	61.9	118	2	PQ0366	Ig heavy chain v r
28	463.5	61.6	114	2	S11099	Ig heavy chain v r
29	463.5	61.6	127	2	B31807	Ig heavy chain v r

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:25 ; Search time 66.1503 Seconds
(without alignments)
1999.647 Million cell updates/sec

Title: US-10-724-274-16

Perfect score: 752
Sequence: 1 MAVGLLLCLVTPFSCVLSQ.....TTTGDALDYWGQCTSVTVSS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.2*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	594	79.0	484	Q5U472_MOUSE	Q5U472 mus musculus
2	580.5	77.2	144	HV43_MOUSE	P01819 mus musculus
3	568	75.5	482	Q91X92_MOUSE	Q91X92 mus musculus
4	548	72.9	591	Q51019_RAT	Q51019 rattus norv
5	537.5	71.5	469	Q5M839_RAT	Q5M839 rattus norv
6	529.5	70.4	477	Q51011_RAT	Q51011 rattus norv
7	521.5	69.3	458	Q5M842_RAT	Q5M842 rattus norv
8	519	69.0	115	HV44_MOUSE	P01820 mus musculus
9	497	66.1	116	HV45_MOUSE	P01821 mus musculus
10	481	64.0	121	Q99NG4_MOUSE	Q99NG4 mus musculus
11	400	53.2	485	Q561M5_MOUSE	Q561M5 mus musculus
12	399.5	53.1	483	Q5U413_MOUSE	Q5U413 mus musculus
13	398.5	53.0	135	HV02_XENLA	P20957 xenopus lae
14	397.5	52.9	487	Q58E53_MOUSE	Q58E53 mus musculus
15	395.5	52.6	560	Q4V801_XENLA	Q4V801 xenopus lae
16	385.5	51.3	476	Q6GMX1_MOUSE	Q6GMX1 homo sapien
17	385.5	51.3	485	Q58E54_MOUSE	Q58E54 mus musculus
18	384	51.1	617	Q569B3_RAT	Q569B3 rattus norv
19	379	50.4	477	Q6GMX7_HUMAN	Q6GMX7 homo sapien
20	377	50.1	465	Q6GMX6_HUMAN	Q6GMX6 homo sapien
21	377	50.1	615	Q569B6_RAT	Q569B6 rattus norv
22	373.5	49.7	136	HV01_XENLA	P20956 xenopus lae
23	372	49.5	496	Q56KX8_HUMAN	Q56KX8 homo sapien
24	371.5	49.4	136	Q6LR05_MOUSE	Q6LR05 mus musculus
25	371.5	49.4	573	Q8WU38_HUMAN	Q8WU38 homo sapien
26	368.5	49.0	493	Q569J1_HUMAN	Q569J1 homo sapien
27	368	48.9	576	Q5P418_HUMAN	Q5P418 homo sapien
28	368	48.9	620	Q56EY0_HUMAN	Q56EY0 homo sapien
29	366	48.7	137	HV46_MOUSE	P01822 mus musculus
30	365	48.5	482	Q5VLK6_RAT	Q5VLK6 rattus norv
31	361	48.0	478	Q7Z379_HUMAN	Q7Z379 homo sapien

32 360.5 47.9 595 2 Q3B8R4_RAT
33 356 47.3 478 2 Q5FVQ3_RAT
34 356 47.3 479 2 Q99M22_MOUSE
35 355 47.2 150 2 Q95973_HUMAN
36 355 47.2 467 2 Q4VBH1_RAT
37 355 47.2 590 2 Q569B8_RAT
38 354.5 47.1 119 2 Q9UL73_HUMAN
39 354 47.1 472 2 Q6N089_HUMAN
40 352.5 46.9 121 1 HV3U_HUMAN
41 352 46.8 469 2 Q569F4_HUMAN
42 350.5 46.6 240 2 Q652C9_MOUSE
43 350 46.5 118 2 Q811U5_MOUSE
44 347.5 46.2 485 2 Q6PD88_MOUSE
45 347 46.1 136 1 HV16_MOUSE

ALIGNMENTS

RESULT 1

Q5U472_MOUSE
ID Q5U472_MOUSE PRELIMINARY; PRT; 484 AA.
AC Q5U472;
DT 07-DEC-2004, integrated into UniprotKB/TREMBL.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE LOC544903 protein.
GN Name=LOC544903;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; BC085241; AAH85241.1; -; mRNA.
DR Ensembl; ENSMUSG00000054328; Mus musculus.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:11 ; Search time 51.8517 Seconds

(without alignments)
1199.218 Million cell updates/sec

Title: US-10-724-274-20

Perfect score: 722

Sequence: 1 MAVGLLLCLVTFPPSCVLSQ.....HGTYGVTGTDALDYWGQG 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_8.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	722	100.0	136	9 AEB51157	Aeb51157 Chimeric
2	722	100.0	143	8 ADQ31879	Adq31879 Antibody
3	722	100.0	143	8 ADQ31905	Adq31905 Murine an
4	722	100.0	143	8 ADQ31875	Adq31875 Antibody
5	722	100.0	143	8 ADT77638	Adt77638 Antibody
6	722	100.0	143	8 ADT77634	Adt77634 Antibody
7	722	100.0	143	9 AEB51153	Aeb51153 Chimeric
8	722	100.0	143	9 AEB51180	Aeb51180 Chimeric
9	722	100.0	143	9 AED49294	Aed49294 Anti-alpha
10	722	100.0	143	9 AED49290	Aed49290 Anti-alpha
11	627	86.8	124	8 ADT77619	Adt77619 IIAL VH p
12	627	86.8	124	9 AEB51138	Aeb51138 Mouse ant
13	627	86.8	232	8 ADQ31887	Adq31887 Antibody
14	627	86.8	232	8 ADT77646	Adt77646 Antibody
15	627	86.8	232	9 AEB51165	Aeb51165 Chimeric
16	627	86.8	451	8 ADQ31884	Adq31884 Antibody
17	627	86.8	451	8 ADT51712	Adt51712 M200 anti
18	627	86.8	451	8 ADT51711	Adt51711 M200 anti
19	627	86.8	451	8 ADT51709	Adt51709 M200 anti
20	627	86.8	451	8 ADT51713	Adt51713 M200 anti
21	627	86.8	451	8 ADT51710	Adt51710 M200 anti
22	627	86.8	451	8 ADT77643	Adt77643 Antibody
23	627	86.8	451	9 AEB51162	Aeb51162 Chimeric

24	627	86.8	451	10 AEF12090	Aef12090 Anti-alpha
25	627	86.8	451	10 AEF16428	Aef16428 Chimeric
26	627	86.8	451	10 AEF16425	Aef16425 Chimeric
27	627	86.8	451	10 AEF16426	Aef16426 Chimeric
28	627	86.8	451	10 AEF16427	Aef16427 Chimeric
29	627	86.8	451	10 AEF16424	Aef16424 Chimeric
30	560.5	77.6	183	2 AAR15326	Aar15326 IL-2 chim
31	560.5	77.6	183	2 AAR32128	Aar32128 Anti-IL2R
32	551.5	76.4	358	5 AAE27929	Aae27929 Human CH2
33	551.5	76.4	358	6 ABB28338	Abb28338 Antibody
34	551.5	76.4	468	5 AAE27928	Aae27928 Human CSE
35	551.5	76.4	468	6 ABB28337	Abb28337 Antibody
36	550.5	76.2	138	2 AA01146	Aa01146 MAB 10.1
37	550	76.2	135	1 AAP70991	Aap70991 Sequence
38	548.5	76.0	142	4 AAG6520	Aag6520 Mouse ant
39	547	75.8	137	2 AAW30277	Aaw30277 Heavy cha
40	544	75.3	124	8 ADQ31861	Adq31861 Humanised
41	544	75.3	124	8 ADT77620	Adt77620 1 VH pept
42	544	75.3	124	9 AEB51139	Aeb51139 Humanized
43	540.5	74.9	152	2 AAY49210	Aay49210 MAB 1A7 h
44	540.5	74.9	152	2 AAY28469	Aay28469 Heavy cha
45	540.5	74.9	152	2 AAY21546	Aay21546 Monoclonal

ALIGNMENTS

RESULT 1

AEB51157

ID AEB51157 standard; protein; 136 AA.

XX AEB51157;

XX 06-OCT-2005 (first entry)

DE Chimeric alpha-5/beta-1 integrin antibody M200 VH domain.

XX Integrin alpha-5/beta-1; chimeric antibody; antibody engineering;
XX angiogenesis disorder; ocular disease; ophthalmological; antidiabetic;
XX angiogenic; cardiovascular disease; macular degeneration;
XX diabetic retinopathy; retinal neovascularization; vascularization.

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

XX US2005163769-A1.

XX 28-JUL-2005.

XX 23-APR-2004; 2004US-00830956.

XX 26-NOV-2002; 2002US-0429743P.

PR 30-SEP-2003; 2003US-0508149P.

XX 26-NOV-2003; 2003US-00724274.

XX (RAMA/) RAMAKRISHNAN V.

PA (POWE/) POWERS D.

PA (JOHN/) JOHNSON D E.

XX (JEFF/) JEFFERY U.

PI Ramakrishnan V, Powers D, Johnson DE, Jeffery U;

XX WPI; 2005-521374/53.

DR N-PSDB; AEB51156.

XX New chimeric anti-alpha5beta1 integrin antibodyalpha-5/beta-1, useful for
XX treating angiogenesis-associated ocular disease, ocular disease, or a
XX growth factor-associated ocular disease.

PT Claim 1; SEQ ID NO 20; 69pp; English.

XX The invention relates to a novel chimeric anti-alpha-5/beta-1 integrin
CC

RESULT 2
IIS-09-772-103-4

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	584	80.9	144	2	S11244	Ig gamma-2a chain
2	550.5	76.2	144	1	G2MS14	Ig heavy chain pre
3	539	74.7	141	2	S52446	Ig heavy chain V r
4	535.5	74.2	140	2	S55028	Ig heavy chain V r
5	533	73.8	135	2	S31913	Ig gamma-2A chain
6	523	72.4	117	2	S10111	Ig heavy chain V r
7	520	72.0	139	2	A32456	Ig heavy chain pre
8	519	71.9	115	1	HVMS14	Ig heavy chain pre
9	499.5	69.2	140	2	S14238	Ig gamma-1 chain p
10	497	68.8	116	1	G1MS10	Ig heavy chain pre
11	496	68.7	116	2	A33932	Ig mu chain precu
12	477	66.1	101	2	S03466	Ig heavy chain V r
13	473	65.5	117	2	S38563	Ig heavy chain V r
14	473	65.5	122	2	S20809	Ig heavy chain V r
15	465	64.4	122	2	A49049	Ig heavy chain V r
16	460	63.7	120	2	PL0087	Ig heavy chain V r
17	458.5	63.5	112	2	S11100	Ig heavy chain V r
18	454.5	63.0	106	2	S14489	Ig heavy chain V r
19	454.5	63.0	114	2	S11106	Ig heavy chain V r
20	452.5	62.7	114	2	S11099	Ig heavy chain V r
21	448.5	62.1	116	2	S11102	Ig heavy chain V r
22	446.5	61.8	113	2	S11101	Ig heavy chain V r
23	445.5	61.7	111	2	S26324	Ig heavy chain V r
24	445.5	61.7	118	2	PQ0266	Ig heavy chain V r
25	445.5	61.7	231	2	PC4155	Ig gamma-2b chain
26	445	61.6	116	2	S24284	Ig heavy chain V r
27	444	61.5	107	2	S14492	Ig heavy chain V r
28	443.5	61.4	112	2	S11108	Ig heavy chain V r
29	443	61.4	118	2	S32786	Ig heavy chain (a

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:25 ; Search time 62.9122 Seconds
(without alignments)
1999.647 Million cell updates/sec

Title: US-10-724-274-20

Perfect score: 722

Sequence: 1 MAVLGLLLCITFPSCVLSQ.....HGTYGMMTTGDALDYGQG 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	79.4	484	Q5U472_MOUSE	Q5U472 mus musculus
2	550.5	76.2	144	HV43_MOUSE	P01819 mus musculus
3	538	74.5	482	Q91X92_MOUSE	Q91X92 mus musculus
4	528	73.1	591	Q510L9_RAT	Q51019 rattus norv
5	519	71.9	115	HV44_MOUSE	P01820 mus musculus
6	517.5	71.7	469	Q5M839_RAT	Q5M839 rattus norv
7	509.5	70.6	477	Q510J1_RAT	Q510j1 rattus norv
8	501.5	69.5	458	Q5M842_RAT	Q5M842 rattus norv
9	497	68.8	116	HV45_MOUSE	P01821 mus musculus
10	451	62.5	121	Q99NG4_MOUSE	Q99ng4 mus musculus
11	376.5	52.1	135	HV02_XENLA	P20957 xenopus lae
12	373.5	51.7	560	Q4V801_XENLA	Q4v801 xenopus lae
13	370	51.2	485	Q561M5_MOUSE	Q561m5 mus musculus
14	369.5	51.2	483	Q5U413_MOUSE	Q5u413 mus musculus
15	367.5	50.9	487	Q58E53_MOUSE	Q58e53 mus musculus
16	364.5	50.5	485	Q58E54_MOUSE	Q58e54 mus musculus
17	360.5	49.9	476	Q6GMX1_HUMAN	Q6gmxi homo sapien
18	359	49.7	617	Q569B3_RAT	Q569b3 rattus norv
19	357	49.4	615	Q569B6_RAT	Q569b6 rattus norv
20	355	49.2	477	Q6GMX7_HUMAN	Q6gmxi7 homo sapien
21	353	48.9	465	Q6GMX6_HUMAN	Q6gmxi6 homo sapien
22	351.5	48.7	136	HV01_XENLA	P20956 xenopus lae
23	350.5	48.5	136	Q6LQ05_MOUSE	Q6lq05 mus musculus
24	348	48.2	496	Q96KX8_HUMAN	Q96kx8 homo sapien
25	345	47.8	482	Q5VLK6_RAT	Q5vlr6 rattus norv
26	344.5	47.7	573	Q8WU38_HUMAN	Q8wu38 homo sapien
27	344	47.6	620	Q96EY0_HUMAN	Q96ey0 homo sapien
28	343.5	47.6	493	Q569J1_HUMAN	Q569j1 homo sapien
29	342	47.4	137	HV46_MOUSE	P01822 mus musculus
30	341	47.2	576	Q6P4I8_HUMAN	Q6p4i8 homo sapien
31	340.5	47.2	595	Q3B8R4_RAT	Q3b8r4 rattus norv

32 338 46.8 139 2 Q86SX2_HUMAN Q86sx2 homo sapien
33 337 46.7 478 2 Q7Z379_HUMAN Q7z379 homo sapien
34 335 46.4 467 2 Q4VBH1_RAT Q4vbh1 rattus norv
35 335 46.4 479 2 Q99M22_MOUSE Q99m22 mus musculus
36 333.5 46.2 121 1 HV3J_HUMAN P01771 homo sapien
37 332 46.0 116 1 HV61_MOUSE F16532 mus musculus
38 332 46.0 478 2 Q5FVQ3_RAT Q5fvq3 rattus norv
39 331 45.8 590 2 Q569B8_RAT Q569b8 rattus norv
40 330.5 45.8 119 2 Q9UL73_HUMAN Q9ul73 homo sapien
41 330 45.7 150 2 Q95973_HUMAN Q95973 homo sapien
42 329 45.6 118 2 Q811U5_MOUSE Q811u5 mus musculus
43 328 45.4 469 2 Q569F4_HUMAN Q569f4 homo sapien
44 327 45.3 116 1 HV60_MOUSE F18531 mus musculus
45 327 45.3 472 2 Q6N089_HUMAN Q6n089 homo sapien

ALIGNMENTS

RESULT 1

Q5U472_MOUSE PRELIMINARY; PRT; 484 AA.
ID Q5U472_MOUSE
AC Q5U472;
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2006, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE LOC54903 protein.
GN Name=LOC54903;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
RX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RC MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lottner J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

NUCLEOTIDE SEQUENCE.

STRAIN=FVB/N; TISSUE=Colon;
NIH MGC Project;
Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.

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EMBL; BC085241; AAH85241.1; -; mRNA.
DR Ensembl; ENSMUSG0000054328; Mus musculus.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG_v.

us-10-724-274-25.ra1

Tue Jun 6 11:58:15 2006

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:59:30 ; Search time 47.535 Seconds
(without alignments)
830.460 Million cell updates/sec

Title: US-10-724-274-25
Perfect score: 2400
Sequence: 1 QVQLKESGPGLVAPQSLSI.....MHEALHNYTKSLSLGK 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/8_COMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/9_COMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	2072	86.3	443	5	PCT-US96-13152-4
2	2063.5	86.0	467	1	US-08-704-744-81
3	2057	85.7	460	2	US-10-630-406-5
4	2033.5	84.7	467	2	US-08-523-894-8
5	2026.5	84.4	467	2	US-08-523-894-10
6	2021.5	84.2	467	2	US-08-523-894-12
7	2020.5	84.2	446	2	US-08-397-411-7
8	2011.5	83.8	467	1	US-07-916-098A-45
9	1981	82.5	464	2	US-05-472-087-2
10	1981	82.5	464	2	US-09-472-087-66
11	1977	82.4	451	2	US-09-472-087-70
12	1976.5	82.4	463	2	US-09-472-087-4
13	1976.5	82.4	463	2	US-09-472-087-68
14	1970.5	82.1	463	2	US-09-472-087-1
15	1970.5	82.1	463	2	US-09-472-087-64
16	1964.5	81.9	463	2	US-09-472-087-64
17	1951.5	81.3	467	2	US-08-030-175-41
18	1949.5	81.2	473	2	US-09-049-672A-4
19	1947.5	81.1	450	2	US-09-996-288-222
20	1947.5	81.1	450	2	US-09-996-288-224
21	1947.5	81.1	450	2	US-09-996-265-222
22	1947.5	81.1	450	2	US-09-996-265-224
23	1947.5	81.1	467	2	US-08-030-175-42
24	1945.5	81.1	450	2	US-09-996-288-210
25	1945.5	81.1	450	2	US-09-996-288-220
26	1945.5	81.1	450	2	US-09-996-288-238

Sequence 240, App
Sequence 242, App
Sequence 244, App
Sequence 246, App
Sequence 210, App
Sequence 220, App
Sequence 238, App
Sequence 240, App
Sequence 242, App
Sequence 246, App
Sequence 230, App
Sequence 208, App
Sequence 218, App
Sequence 250, App
Sequence 208, App
Sequence 218, App
Sequence 250, App

ALIGNMENTS

RESULT 1
PCT-US96-13152-4
Sequence 4, Application PC/TUS9613152
GENERAL INFORMATION: Martin, Ulrich, et al.
APPLICANT: Anti-selectin antibodies for prevention of multiple organ fa
TITLE OF INVENTION: 4
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Hanson
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 443
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-13152-4
Query Match 86.3%; Score 2072; DB 5; Length 443;
Best Local Similarity 86.7%; Pred. No. 1.5e-152;

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:11 ; Search time 171.949 Seconds
(without alignments)
1199.218 Million cell updates/sec

Title: US-10-724-274-25
Perfect score: 2400
Sequence: 1 QVQLKSGPGLVAPQSLSI.....MHEALNHYTKSLSLGK 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_8:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003s:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*
- 10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2400	100.0	451	8	ADQ31884 Antibody
2	2400	100.0	451	8	ADT77643 Antibody
3	2400	100.0	451	9	AEb51162 Chimeric
4	2400	100.0	451	10	AEf12090 Anti-alpha
5	2397	99.9	451	8	ADT51711 M200 anti
6	2397	99.9	451	10	AEf16426 Chimeric
7	2394	99.8	451	8	ADT51709 M200 anti
8	2394	99.8	451	8	ADT51710 M200 anti
9	2394	99.8	451	10	AEf16425 Chimeric
10	2394	99.8	451	10	AEf16424 Chimeric
11	2391	99.6	451	8	ADT51712 M200 anti
12	2391	99.6	451	10	AEf16427 Chimeric
13	2389	99.5	451	8	ADT51713 M200 anti
14	2389	99.5	451	10	AEf16428 Chimeric
15	2282	95.1	451	8	ADQ31890 Antibody
16	2282	95.1	451	9	AEb51168 Chimeric
17	2165.5	90.2	442	9	ADY74779 Rat anti-
18	2138.5	89.1	442	9	ADY74807 Rat anti-
19	2107.5	87.8	469	9	AEb45853 Human mon
20	2107	87.8	462	9	AEb45881 Human mon
21	2105.5	87.7	469	8	ADs16636 Human ant
22	2100.5	87.5	465	9	AEb45849 Human mon
23	2098.5	87.4	463	9	AEa41030 Human ant

24	2097	87.4	462	8	ADF77154	Adf77154 Chimeric
25	2097	87.4	466	8	ADM41565	Adm41565 Anti-inte
26	2091	87.1	476	4	AB49243	Ab49243 Chimeric
27	2089.5	87.1	444	6	ABR55342	AbR55342 Amino aci
28	2088.5	87.0	446	8	ADK52356	AdK52356 Human ant
29	2084	86.8	464	9	AEC20880	Aec20880 Low risk
30	2082	86.8	468	5	AAE27928	AAe27928 Human C5E
31	2082	86.8	468	6	ABB82837	Abb82837 Antibody
32	2079.5	86.6	489	8	ADL93669	AdL93669 Human CD4
33	2077	86.5	486	8	ADM41559	Adm41559 Anti-inte
34	2074.5	86.4	469	8	ADL93662	AdL93662 Human CD4
35	2072	86.3	443	2	AAW13564	AAw13564 Humanised
36	2072	86.3	464	8	ADL93663	AdL93663 Human CD4
37	2070	86.2	447	9	AEC40039	Aec40039 Heavy cha
38	2070	86.2	462	8	ADL93670	AdL93670 Human CD4
39	2067.5	86.1	461	9	AEA41064	AEa41064 Human ant
40	2067.5	86.1	461	9	AEA41047	AEa41047 Human ant
41	2066.5	86.1	461	9	AEA41062	AEa41062 Human ant
42	2065	86.0	466	8	ADL93667	AdL93667 Human CD4
43	2064.5	86.0	465	7	ADD93783	AdD93783 Monoclona
44	2064.5	86.0	469	8	ADU17617	AdU17617 Human ant
45	2064.5	86.0	469	8	ADU17474	AdU17474 Human ant

ALIGNMENTS

RESULT 1

ADQ31884
ID ADQ31884 standard; protein; 451 AA.

XX AC ADQ31884;

XX DT 23-SEP-2004 (first entry)

XX DE Antibody M200 heavy chain amino acid sequence SEQ ID NO:25.

XX KW chimeric anti-alpha5beta-1 integrin antibody; antibody; immunoreactive;
KW alpha5beta1 integrin; humanised anti-alpha5beta1 integrin antibody;
KW vascularisation; antiangiogenic; integrin alpha5beta1 antagonist.

XX OS Mus sp.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO2004056308-A2.

XX PD 08-JUL-2004.

XX PF 26-NOV-2003; 2003WO-US038172.

XX PR 26-NOV-2002; 2002US-0429743P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Ramakrishnan V, Powers D, Johnson DE, Jeffrey U;

XX DR WPI; 2004-525316/50.

XX DR N-PSDB; ADQ31882.

XX PT New chimeric anti-alpha-5 beta-1 integrin antibody useful for controlling
vascularization in injured tissue.

XX PS Claim 23; SEQ ID NO 25; 89pp; English.

XX CC The present invention describes a chimeric anti-alpha5beta-1 integrin
antibody (I), comprising: (a) a first polypeptide sequence from a first
source comprising one or more amino acid sequences selected from SEQ ID
NOs: 1, 7, 16, 18, 20, 22, 25, 26, 28, 31 and 32; and (b) a second
polypeptide from a second source comprising a constant region sequence of
an antibody of the second source, where the first and second polypeptide
sequences form a protein complex that is immunoreactive with alpha5beta1
integrin. Also described: (1) purifying (M1) pH-sensitive (I) comprises

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:47:35 ; Search time 26.9954 Seconds
(without alignments)
1607.447 Million cell updates/sec

Title: US-10-724-274-25
Perfect score: 2400
Sequence: 1 QVQLKESGGLVAPSSQSLSI.....MHEALHNHYTQKSLSLGLK 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1743	72.6	327	1 G4HU	Ig gamma-4 chain C
2	1605.5	66.9	326	1 G2HU	Ig gamma-2 chain C
3	1590.5	66.3	330	1 GHU	Ig gamma-1 chain C
4	1585	65.0	377	2 A60764	Ig gamma-3 chain C
5	1575	65.6	377	2 A23511	Ig gamma-3 chain C
6	1554	64.8	470	2 S22080	Ig heavy chain pre
7	1519	63.3	472	2 P43459	Ig gamma-1 chain -
8	1423.5	59.3	444	2 P4436	monoclonal antibody
9	1417	59.0	446	2 S40295	Ig gamma-2a chain
10	1412.5	58.9	469	2 S37483	Ig gamma-2a chain
11	1411	58.8	374	2 S93339	Ig heavy chain v r
12	1305	54.4	474	1 G2MS11	Ig gamma-2b chain
13	1289.5	53.7	328	2 I47159	Ig gamma 2a chain
14	1289.5	53.7	475	2 S01321	Ig gamma-2b chain
15	1283.5	53.5	328	2 I47160	Ig gamma 2b chain
16	1264.5	52.7	328	2 I47161	Ig gamma 1 chain c
17	1240.5	51.7	328	2 I47158	Ig gamma 1 chain c
18	1199	50.0	323	1 GHRB	Ig gamma chain C r
19	1162	48.4	329	1 G3GP	Ig gamma-2 chain C
20	1147	47.8	308	2 C30554	Ig heavy chain C r
21	1139.5	47.5	255	4 S31866	Ig gamma-1 chain C
22	1139.5	47.1	234	2 PT0207	Ig gamma chain C r
23	1124	46.8	333	2 P80018	Ig gamma-2b chain C
24	1118.5	46.6	326	2 P80017	Ig gamma-1 chain C
25	1108.5	46.2	289	1 G3HUW1	Ig gamma-3 heavy c
26	1108	46.2	329	2 S00847	Ig gamma-2c chain
27	1106.5	46.1	324	1 GLMS	Ig gamma-1 chain C
28	1106.5	46.1	330	1 G2MSA	Ig gamma-2a chain
29	1103	46.0	327	2 S06611	Ig gamma-2 chain C

30	1101.5	45.9	393	1 G1MSM	Ig gamma-1 chain C
31	1101.5	45.9	399	1 G2MSAM	Ig gamma-2a chain
32	1099	45.8	335	1 G2MSAB	Ig gamma-2a chain
33	1098.5	45.8	229	1 G3MSC	Ig gamma-3 chain C
34	1090.5	45.4	398	1 G3MSM	Ig gamma-3 chain C
35	1085.5	45.2	277	2 I47162	Ig gamma 4 chain c
36	1084.5	45.2	322	2 P80019	Ig gamma-2a chain
37	1049.5	43.7	405	1 G2MSBM	Ig gamma-2b chain
38	942	39.2	548	2 S38864	Ig epsilon chain C
39	845.5	35.2	549	2 S04845	Ig heavy chain pre
40	797	33.2	231	2 PC4155	Ig gamma-2b chain
41	790.5	32.9	241	2 S69131	Ig heavy chain (DO
42	785.5	32.7	220	2 A49444	Ig gamma-1 heavy c
43	769.5	32.1	572	2 B46529	Ig y heavy chain (
44	760	31.7	592	2 S25705	Ig mu chain - shee
45	749.5	31.2	249	2 S69340	Ig heavy chain VHI

ALIGNMENTS

RESULT 1

G4HU
IG gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90333; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
A;Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into : C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMI>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) #status predicted

Query Match	72.6%	Score 1743;	DB 1;	Length 327;
Best Local Similarity	100.0%;	Pred. No. 5.5e-95;		
Matches 327;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	125	ASTKGPSVFPLAPCSRTSSTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	184	
Db	1	ASTKGPSVFPLAPCSRTSSTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	60	
Qy	185	GLYSLSSVTVTPSSSLGTTKTYTCNVDRHKPSNTKVDKRVESKYGGPPCPSCPAPEFLGGPSV	244	
Db	61	GLYSLSSVTVTPSSSLGTTKTYTCNVDRHKPSNTKVDKRVESKYGGPPCPSCPAPEFLGGPSV	120	

Result No.	Query			ID	Description
	Score	Match	Length		
1	2041.5	85.1	476	2	Q6MZX7 HUMAN
2	2014	83.9	473	2	Q8TC63 HUMAN
3	1948	81.2	472	2	Q6GMX1 HUMAN
4	1943	81.0	472	2	Q6N089 HUMAN
5	1939.5	80.8	465	2	Q6GMX6 HUMAN
6	1939.5	80.8	469	2	Q569F4 HUMAN
7	1918	79.9	478	2	Q6P181 HUMAN
8	1916	79.8	470	2	Q6PJ4A HUMAN
9	1914.5	79.8	465	2	Q6P6C4 HUMAN
10	1912	79.7	464	2	Q6MZU6 HUMAN
11	1905	79.4	466	2	Q6IN78 HUMAN
12	1902	79.2	470	2	Q725W1 HUMAN
13	1900.5	79.2	475	2	Q5EPF5 HUMAN
14	1896.5	79.0	544	2	Q6PU95 HUMAN
15	1894	78.9	470	2	Q68CN4 HUMAN
16	1891.5	78.8	473	2	Q6MZV7 HUMAN
17	1891	78.8	482	2	Q72351 HUMAN
18	1886	78.6	480	2	Q6N094 HUMAN
19	1882.5	78.4	475	2	Q6GMW7 HUMAN
20	1877.5	78.2	481	2	Q6N097 HUMAN
21	1877	78.2	466	2	Q6N096 HUMAN
22	1870.5	77.9	475	2	Q6MQZ6 HUMAN
23	1869.5	77.9	475	2	Q6N095 HUMAN
24	1866.5	77.8	473	2	Q6P055 HUMAN
25	1856.5	77.4	521	2	Q8N4Y9 HUMAN
26	1851.5	77.1	519	2	Q5EBM2 HUMAN
27	1848	77.0	417	2	Q6N093 HUMAN
28	1838	76.6	518	2	Q6N030 HUMAN
29	1829	76.2	480	2	Q6PJF1 HUMAN
30	1821.5	75.9	469	2	Q727P5 HUMAN
31	1820.5	75.9	475	2	O5RE17 PONYA

[illegible]

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:11 ; Search time 88.4528 Seconds
(without alignments)
1199.218 Million cell updates/sec

Title: US-10-724-274-28
Perfect score: 1225
Sequence: 1 QVQLKESGPGLVAPSSQSLSI.....PSNTKVDKRVESKIGPPCPSS 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq18:
1: Geneseq1980s:
2: Geneseq1990s:
3: Geneseq2000s:
4: Geneseq2001s:
5: Geneseq2002s:
6: Geneseq2003as:
7: Geneseq2003bs:
8: Geneseq2004s:
9: Geneseq2005s:
10: Geneseq2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result, being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	100.0	232	8 ADQ31887	Adg31887 Antibody
2	1225	100.0	232	8 ADT77646	Adt77646 Antibody
3	1225	100.0	232	8 AEB51165	Aeb51165 Chimeric
4	1225	100.0	451	8 ADQ31884	Adg31884 Antibody
5	1225	100.0	451	8 ADT51712	Adt51712 M200 anti
6	1225	100.0	451	8 ADT51711	Adt51711 M200 anti
7	1225	100.0	451	8 ADT51709	Adt51709 M200 anti
8	1225	100.0	451	8 ADT51713	Adt51713 M200 anti
9	1225	100.0	451	8 ADT51710	Adt51710 M200 anti
10	1225	100.0	451	8 ADT77643	Adt77643 Antibody
11	1225	100.0	451	9 AEB51162	Aeb51162 Chimeric
12	1225	100.0	451	9 AEF12090	Aef12090 Anti-alph
13	1225	100.0	451	10 AEF16428	Aef16428 Chimeric
14	1225	100.0	451	10 AEF16425	Aef16425 Chimeric
15	1225	100.0	451	10 AEF16426	Aef16426 Chimeric
16	1225	100.0	451	10 AEF16427	Aef16427 Chimeric
17	1225	100.0	451	10 AEF16424	Aef16424 Chimeric
18	1107	90.4	451	8 ADQ31890	Adg31890 Antibody
19	1107	90.4	451	9 AEB51168	Aeb51168 Chimeric
20	997	81.4	462	8 ADT74779	Adt74779 Rat anti-
21	990.5	80.9	442	9 ADT74775	Adt74775 Chimeric
22	981.5	80.1	476	4 AAB49243	Aab49243 Chimeric
23	978.5	79.9	468	5 AAE27928	Aae27928 Human CSE

24	978.5	79.9	468	6 ABB82837	Abb82837 Antibody
25	977.5	79.8	358	5 AAE27929	Aae27929 Human CH2
26	977.5	79.8	358	6 ABB82838	Abb82838 Antibody
27	963.5	78.7	442	9 ADY74807	Ady74807 Rat anti-
28	963	78.6	241	2 AAR21261	Aar21261 VHD1.3-Hu
29	961	78.4	469	8 ADU17617	Adul7617 Human ant
30	961	78.4	469	8 ADU17474	Adul7474 Human ant
31	956	78.0	446	9 AEA48170	Aea48170 Mouse ant
32	943.5	77.0	468	8 ADS14299	Adsl14299 EGFR anti
33	935.5	76.4	782	8 ADP44637	Adp44637 Murine an
34	935.5	76.4	782	8 AEA60463	Aea60463 Mouse ant
35	932.5	76.1	469	9 AEB45853	Aeb45853 Human mon
36	932.5	76.1	462	9 AEB45881	Aeb45881 Human mon
37	932	76.1	462	9 AEB45881	Aeb45881 Human mon
38	931	76.0	447	8 ADQ17121	Adq17121 Humanised
39	930.5	76.0	463	9 AEA41030	Aea41030 Human ant
40	930.5	76.0	465	9 AEB45849	Aeb45849 Human mon
41	930.5	76.0	469	8 ADS16636	Adsl16636 Human ant
42	929	75.8	466	8 ADM41565	Adm41565 Anti-inte
43	925.5	75.6	220	10 AEF22802	Aef22802 Cetuximab
44	925	75.5	581	4 AAB81972	Aab81972 Gangliosid
45	922	75.3	254	8 ADQ98104	Adq98104 Chimeric

ALIGNMENTS

RESULT 1

ADQ31887

ID ADQ31887 standard; protein; 232 AA.
XX ADQ31887;
AC ADQ31887;
XX
DT 23-SEP-2004 (first entry)
XX
DB Antibody F200 heavy chain amino acid sequence SEQ ID NO:28.
XX
KW chimeric anti-alpha5beta-1 integrin antibody; antibody; immunoreactive;
KW alpha5beta1 integrin; humanised anti-alpha5beta1 integrin antibody;
KW vascularisation; antiangiogenic; integrin alpha5beta5 antagonist.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
XX
FN WO2004056308-A2.
XX
PD 08-JUL-2004.
XX
PF 26-NOV-2003; 2003WO-US038172.
XX
PR 26-NOV-2002; 2002US-0429743P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Ramakrishnan V, Powers D, Johnson DB, Jeffrey U;
XX
DR WPI; 2004-525316/50.
XX
DR N-PSDB; ADQ31886.
XX
PT New chimeric anti-alpha-5 beta-1 integrin antibody useful for controlling
PT vascularisation in injured tissue.
XX
PS Claim 23; SEQ ID NO 28; 89pp; English.
XX
CC The present invention describes a chimeric anti-alpha5beta-1 integrin
CC antibody (I), comprising: (a) a first polypeptide sequence from a first
CC source comprising one or more amino acid sequences selected from SEQ ID
CC NOS: 1, 7, 16, 18, 20, 22, 25, 26, 28, 31 and 32; and (b) a second
CC polypeptide from a second source comprising a constant region sequence of
CC an antibody of the second source, where the first and second polypeptide
CC sequences form a protein complex that is immunoreactive with alpha5beta1
CC integrin. Also described: (1) purifying (M1) pH-sensitive (I) comprises

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:47:35 ; Search time 13.886 Seconds
(without alignments)

1607.447 Million cell updates/sec

Title: US-10-724-274-28

Perfect score: 1225

Sequence: 1 QVQLKESGPGLVAPQSLSL.....PSNTKVDKRVESKYGPPCPFS 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.* ;

1: Piri.* ;

2: Piri.* ;

3: Piri.* ;

4: Piri.* ;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	789	64.4	231	PC4155	Ig gamma-2b chain
2	785.5	64.1	220	A49444	Ig gamma-1 heavy c
3	750.5	61.3	241	S69131	Ig heavy chain (DO
4	721	58.9	470	S22080	Ig heavy chain pre
5	694	56.7	472	S31459	Ig gamma-1 chain -
6	660	53.9	246	S38950	Ig gamma chain - m
7	660	53.9	446	S40295	Ig gamma-2a chain
8	640.5	52.3	469	S37483	Ig gamma-2a chain
9	631.5	51.6	444	PC4436	monoclonal antibody
10	626.5	51.1	220	S68211	Ig heavy chain (Ma
11	620.5	50.7	548	S38864	Ig epsilon chain C
12	611	49.9	213	S68213	Ig heavy chain (Ma
13	578.5	47.2	475	S01321	Ig gamma-2b chain
14	577	47.1	221	PC4220	Ig gamma-1 chain -
15	575.5	47.0	214	S42002	monoclonal antibody
16	573.5	46.8	254	S31790	Ig heavy chain v r
17	568	46.4	327	G4HU	Ig gamma-4 chain C
18	567	46.3	474	G2MS11	Ig gamma-2b chain
19	552	45.1	549	S04845	Ig heavy chain pre
20	529	43.2	144	S11244	Ig gamma-2a chain
21	513.5	41.9	326	G2HU	Ig gamma-2 chain C
22	508.5	41.5	140	S14238	Ig gamma-1 chain p
23	503	41.1	122	S20809	Ig heavy chain v r
24	501	40.9	377	A23511	Ig gamma-3 chain C
25	501	40.9	377	A23511	Ig gamma-3 chain C
26	500.5	40.9	144	G2MS14	Ig heavy chain pre
27	499	40.7	117	S38563	Ig heavy chain v r
28	498	40.7	122	A49049	Ig heavy chain v r
29	496	40.5	592	S25705	Ig mu chain - shee

ALIGNMENTS

RESULT 1

PC4155

Ig gamma-2b chain V-C region MabB23 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000

C/Accession: PC4155

R/Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.

Gene 189, 237-239, 1996

A/Title: Cloning and characterization of cDNAs coding for heavy and light chains of a n

A/Reference number: PC4155; MUID:96194809; PMID:8647454

A/Accession: PC4155

A/Molecule type: mRNA

A/Residues: 1-231 <KWA>

A/Cross-references: UNIPARC:UPI00001157CB; GB:U28970; NID:G1262180; PIDN:AAC52489.1; P;

A/Note: This protein has unusual amino acid compared with the conserved sequences of m

C/Superfamily: immunoglobulin C region; immunoglobulin homology

F/1-231/Product: heavy chain #status predicted <MAT>

F/98-102/Region: unique D sequence

F/103-119/Region: V region

F/139-203/Domain: immunoglobulin homology <IMM>

Query Match 64.4%; Score 789; DB 2; Length 231;

Best Local Similarity 66.5%; Pred. No. 1.9e-47;

Matches 157; Conservative 26; Mismatches 41; Indels 12; Gaps 4;

Qy	1	QVQLKESGPGLVAPQSLSITCTISGFSITDYGVHVRQPPGKGLVWLVIWSDGSSSTYN	60
Db	1	EVQLVESGPGLVAPQSLSITCTVSGFSLTDYGVSWIRQPPGKGLVWLVIWAGSGSTFYN	60
Qy	61	SALKSRMTIRKDNKSQVFLIMNSLOTDDSAMVYCARHGTYYGTTTTGDALDYWGQGTSV	120
Db	61	SALKSRSLINKDNKSQVFLKNSLHTDDTANYICVHEDRYDW-----YFDVWGAGITV	115
Qy	121	TVSSASTKGPSVPLPCRSRSTSESTAALGLVXDYPPEPTVTVSNWNSGALSGVHTTPAV	180
Db	116	TVSSAKTPPSVPLAPRCGDTTGSVTLGLVKGYPPESTVTWNSGSLSSSVHTFPAL	175
Qy	181	LQSSGLVSLSSVTVTPSSSLGTQTYTCNVDPKPNKVDKRVESKYGP-----PCP	231
Db	176	LQ-SGLYTMSSSVTVPSSTWPSQTVCVAHPASSTTVDKKLEPS-GPSTINPCP	229

RESULT 2

A49444

Ig gamma-1 heavy chain (New) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 16-Jul-1999

C/Accession: A49444

R/Saul, F.A.; Poljak, R.J.

Proteins 14, 363-371, 1992

A/Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A r

A/Reference number: A49444; MUID:93066153; PMID:1438175

GenCore version 5.1.9
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CM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:25 ; Search time 107.321 Seconds
(without alignments)
1999.647 Million cell updates/sec

Title: US-10-724-274-28

Fact score: 1225

Sequence: 1 QVQLKESGGLVAPSSQSLST.....PSNTKYDKRVESKYGPCCPS 232

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	875.5	71.5	476	Q6MXZ7_HUMAN	Q6mxz7 homo sapien
2	844.5	68.9	476	Q6GKH1_HUMAN	Q6gmkl homo sapien
3	839.5	68.5	472	Q6N089_HUMAN	Q6n089 homo sapien
4	839	68.5	473	Q8TC63_HUMAN	Q8tc63 homo sapien
5	836	68.2	465	Q6GMX6_HUMAN	Q6gmx6 homo sapien
6	836	68.2	469	Q569F4_HUMAN	Q569f4 homo sapien
7	827.5	67.6	465	Q6P6C4_HUMAN	Q6p6c4 homo sapien
8	823	67.2	464	Q6MZU6_HUMAN	Q6mzu6 homo sapien
9	816	66.6	470	Q68CN4_HUMAN	Q68cn4 homo sapien
10	812.5	66.3	470	Q6PJ44_HUMAN	Q6pj44 homo sapien
11	808.5	66.0	478	Q6PI81_HUMAN	Q6pi81 homo sapien
12	801.5	65.4	466	Q6IN78_HUMAN	Q6in78 homo sapien
13	801	65.4	544	Q6PJ95_HUMAN	Q6pj95 homo sapien
14	798.5	65.2	470	Q7Z5W1_HUMAN	Q7z5w1 homo sapien
15	797	65.1	475	Q5EFES_HUMAN	Q5efes homo sapien
16	791.5	64.6	482	Q7Z351_HUMAN	Q7z351 homo sapien
17	788	64.3	469	Q5M839_RAT	Q5m839 rattus norv
18	786.5	64.2	480	Q6N094_HUMAN	Q6n094 homo sapien
19	782	63.8	473	Q6MZV7_HUMAN	Q6mzv7 homo sapien
20	780.5	63.7	466	Q6N096_HUMAN	Q6n096 homo sapien
21	779.5	63.6	521	Q8N4Y9_HUMAN	Q8n4y9 homo sapien
22	779	63.6	475	Q6GMW7_HUMAN	Q6gmw7 homo sapien
23	778	63.5	481	Q6N097_HUMAN	Q6n097 homo sapien
24	777.5	63.5	519	Q5EBM2_HUMAN	Q5ebm2 homo sapien
25	777	63.4	475	Q6N095_HUMAN	Q6n095 homo sapien
26	772	63.0	458	Q5M842_RAT	Q5m842 rattus norv
27	771	62.9	475	Q5M206_HUMAN	Q5m206 homo sapien
28	767	62.6	473	Q6P055_HUMAN	Q6p055 homo sapien
29	764	62.4	518	Q6N030_HUMAN	Q6n030 homo sapien
30	756	61.7	417	Q6N093_HUMAN	Q6n093 homo sapien
31	733	59.8	475	Q5RE17_PONPY	Q5re17 pongo pygma

32	719.5	58.7	480	2	Q6PJF1_HUMAN	Q6pjf1 homo sapien
33	718	58.6	469	2	Q7Z7P5_HUMAN	Q7z7p5 homo sapien
34	675.5	55.1	467	2	Q4VBH1_RAT	Q4vbh1 rattus norv
35	665.5	54.3	237	1	HVCM5_MOUSE	Hvcm5 mus musculus
36	653.5	53.3	461	2	Q5M7V3_RAT	Q5m7v3 rattus norv
37	645.5	52.7	471	2	Q66K04_MOUSE	Q66k04 mus musculus
38	642	52.4	468	2	Q569B4_RAT	Q569b4 rattus norv
39	641.5	52.4	473	2	Q91205_MOUSE	Q91205 mus musculus
40	639	52.2	560	2	Q4V801_XENLA	Q4v801 xenopus lae
41	636.5	52.0	465	2	Q510J0_RAT	Q510j0 rattus norv
42	631	51.5	458	2	Q5BUZ2_RAT	Q5bu22 rattus norv
43	628.5	51.3	473	2	Q9DBL4_MOUSE	Q9dbl4 mus musculus
44	627	51.2	464	2	Q6PIP8_MOUSE	Q6pip8 mus musculus
45	626	51.1	468	2	Q569W9_MOUSE	Q569w9 mus musculus

ALIGNMENTS

RESULT 1

Q6MXZ7_HUMAN PRELIMINARY; PRT; 476 AA.

AC Q6MXZ7;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE Hypothetical protein DKFZp686M24218.

GN Name=DKFZp686M24218;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Human rectum tumor;

RG The German Human cDNA Consortium;

RA Bloembergen H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,

RA Fobo G., Han M., Wiemann S.,

RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

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ENBL; BX640824; CAA45900.1; -; mRNA.

DR HSP; P01861; IADQ.

DR SMR; Q6MXZ7; 28-472.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; C1-set; 3.

DR SMART; SM00409; IG; 1.

DR SMART; SM00407; IGC1; 2.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

KW Hypothetical protein.

SQ SEQUENCE 476 AA; 52420 MW; 0D3D1FPE5853958F CRC64;

Query Match 71.5%; Score 875.5; DB 2; Length 476;

Best Local Similarity 71.8%; Pred. No. 1.5e-66;

Matches 169; Conservative 24; Mismatches 37; Indels 5; Gaps 2;

Qy 1 QVQLKESGGLVAPSSQSLSTITGSLTDYGVH--WVRPPGKGLWLVWISDGSST 58

Db 27 QLQLQSGGLVAPSSQSLSTITGSLTDYGVH--WVRPPGKGLWLVWISDGSST 86

Qy 59 YNSALKSRMTIRKDNKSKSVQLFMNSLQTDSDSAMYYCARHGYGMMTTGDALDYWGCGT 118

Db 87 YTSLSKSLRTHVDPSKSKQIFLNLTSVTAADTAVYCVRHG---GYSFASAYPFPFGQA 143

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:11 ; Search time 171.949 Seconds
(without alignments)
1199.218 Million cell updates/sec

Title: US-10-724-274-31

Perfect score: 2399

Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHNYTKSLSLGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq.8:

- 1: Geneseqp1980s*
- 2: Geneseqp1980s*
- 3: Geneseqp2000s*
- 4: Geneseqp2001s*
- 5: Geneseqp2002s*
- 6: Geneseqp2003as*
- 7: Geneseqp2003bs*
- 8: Geneseqp2004s*
- 9: Geneseqp2005s*
- 10: Geneseqp2006s*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2399	100.0	451	ADQ31890	Adq31890 Antibody
2	2399	100.0	451	AEb51168	AEb51168 Chimeric
3	2282	95.1	451	ADQ31884	Adq31884 Antibody
4	2282	95.1	451	ADT77643	Adt77643 Antibody
5	2282	95.1	451	AEb51162	AEb51162 Chimeric
6	2282	95.1	451	AEf12090	AEf12090 Anti-alph
7	2279	95.0	451	ADT51711	ADT51711 M200 anti
8	2279	95.0	451	AEf16426	AEf16426 Chimeric
9	2276	94.9	451	ADT51709	ADT51709 M200 anti
10	2276	94.9	451	ADT51710	ADT51710 M200 anti
11	2276	94.9	451	AEf16425	AEf16425 Chimeric
12	2276	94.9	451	AEf16424	AEf16424 Chimeric
13	2273	94.7	451	ADT51712	ADT51712 M200 anti
14	2273	94.7	451	AEf16427	AEf16427 Chimeric
15	2271	94.7	451	ADT51713	ADT51713 M200 anti
16	2271	94.7	451	AEf16428	AEf16428 Chimeric
17	2206.5	92.0	444	AEb55342	AEb55342 Amino aci
18	2199.5	91.7	469	AEb45881	AEb45881 Human mon
19	2199.5	91.7	469	ADSL6636	ADSL6636 Human ant
20	2192.5	91.4	463	AEb41030	AEb41030 Human ant
21	2189	91.2	443	AEb413564	AEb413564 Humanised
22	2188.5	91.2	469	AEb45853	AEb45853 Human mon
23	2187.5	91.2	469	ADL93669	ADL93669 Human CD4

24	2186.5	91.1	465	9	AEb45849	AEb45849 Human mon
25	2183	91.0	466	8	ADM41565	ADM41565 Anti-inte
26	2182.5	91.0	469	8	ADL93662	ADL93662 Human CD4
27	2177	90.7	464	8	ADL93663	ADL93663 Human CD4
28	2175	90.7	447	9	AEC40039	AEC40039 Heavy cha
29	2172.5	90.6	465	7	ADD93783	ADD93783 Monoclonal
30	2172	90.5	466	8	ADM41559	ADM41559 Anti-inte
31	2170	90.5	462	8	ADL93667	ADL93667 Human CD4
32	2170	90.5	466	8	ADL93667	ADL93667 Human CD4
33	2169.5	90.4	461	9	AEb41064	AEb41064 Human ant
34	2169.5	90.4	461	9	AEb41047	AEb41047 Human ant
35	2168	90.4	460	8	ADL93664	ADL93664 Human CD4
36	2166.5	90.3	467	2	AAR80617	AAR80617 Anti-huma
37	2166	90.3	460	8	ADJ55026	ADJ55026 Plasmid p
38	2165	90.2	462	8	ADL93660	ADL93660 Human CD4
39	2164.5	90.2	461	9	AEb41056	AEb41056 Human ant
40	2164.5	90.2	461	9	AEb41055	AEb41055 Human ant
41	2164	90.2	468	8	ADL93666	ADL93666 Human CD4
42	2161	90.1	462	8	ADL93668	ADL93668 Human CD4
43	2160.5	90.1	461	9	AEb41062	AEb41062 Human ant
44	2160	90.0	464	8	ADL93661	ADL93661 Human CD4
45	2159.5	90.0	467	9	AEb41068	AEb41068 Human ant

ALIGNMENTS

RESULT 1

ADQ31890
ID ADQ31890 standard; protein; 451 AA.

XX AC ADQ31890;

XX DT 23-SEP-2004 (first entry)

DE Antibody hum200 heavy chain amino acid sequence SEQ ID NO:31.

XX chimeric anti-alpha5beta-1 integrin antibody; antibody; immunoreactive;
KW alpha5beta1 integrin; humanised anti-alpha5beta1 integrin antibody;
KW vascularisation; antiangiogenic; integrin alpha5beta5 antagonist.

OS Mus sp.

OS Homo sapiens.

OS Synthetic.

XX FN WO2004056308-A2.

XX PD 08-JUL-2004.

XX PF 26-NOV-2003; 2003WO-US038172.

XX PR 26-NOV-2002; 2002US-0429743P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Ramakrishnan V, Powers D, Johnson DE, Jeffrey U;

XX DR WPI; 2004-525316/50.

XX DR N-PSDB; ADQ31888.

XX PT New chimeric anti-alpha-5 beta-1 integrin antibody useful for controlling

XX PS vascularization in injured tissue.

XX PS Claim 23; SEQ ID NO 31; 89pp; English.

XX CC The present invention describes a chimeric anti-alpha5beta-1 integrin
CC antibody (I), comprising: (a) a first polypeptide sequence from a first
CC source comprising one or more amino acid sequences selected from SEQ ID
CC NOS: 1, 7, 16, 18, 20, 22, 25, 26, 28, 31 and 32; and (b) a second
CC polypeptide from a second source comprising a constant region sequence of
CC an antibody of the second source, where the first and second polypeptide
CC sequences form a protein complex that is immunoreactive with alpha5beta1
CC integrin. Also described: (1) purifying (M1) pH-sensitive (I) comprises

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:59:30 ; Search time 47.5355 Seconds
(without alignments)
830.460 Million cell updates/sec

Title: US-10-724-274-31

Perfect score: 2399
Sequence: 1 EVOLVESGGLVQPGSLRL.....MPEALHHVTKSLSLGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2189	91.2	443	PCT-US96-13152-4	Sequence 4, Appli
2	2166.5	90.3	467	US-08-704-744-81	Sequence 81, Appli
3	2166	90.3	460	US-10-630-406-5	Sequence 5, Appli
4	2067.5	86.2	467	US-07-916-098A-45	Sequence 45, Appli
5	2066	86.1	464	US-09-472-087-2	Sequence 2, Appli
6	2066	86.1	464	US-09-472-087-66	Sequence 66, Appli
7	2063	86.0	451	US-09-472-087-70	Sequence 70, Appli
8	2058.5	85.8	463	US-09-472-087-4	Sequence 4, Appli
9	2058.5	85.8	463	US-09-472-087-68	Sequence 68, Appli
10	2053.5	85.6	463	US-09-472-087-1	Sequence 1, Appli
11	2053.5	85.6	463	US-09-472-087-63	Sequence 63, Appli
12	2047.5	85.3	463	US-09-472-087-64	Sequence 64, Appli
13	2034.5	84.8	467	US-08-523-89A-8	Sequence 8, Appli
14	2033	84.7	451	US-09-925-179-66	Sequence 66, Appli
15	2032	84.7	470	US-09-859-053-32	Sequence 32, Appli
16	2032	84.7	470	US-09-859-053-36	Sequence 36, Appli
17	2032	84.7	474	US-09-848-832-3	Sequence 3, Appli
18	2031.5	84.7	444	US-10-147-849-7	Sequence 7, Appli
19	2030	84.6	451	US-08-887-352B-14	Sequence 14, Appli
20	2030	84.6	451	US-08-887-352B-16	Sequence 16, Appli
21	2030	84.6	451	US-08-466-151-65	Sequence 65, Appli
22	2030	84.6	451	US-09-109-207C-14	Sequence 14, Appli
23	2030	84.6	451	US-09-109-207C-16	Sequence 16, Appli
24	2030	84.6	451	US-09-296-005-14	Sequence 14, Appli
25	2030	84.6	451	US-09-296-005-16	Sequence 16, Appli
26	2030	84.6	451	US-09-920-171-14	Sequence 14, Appli

27	2030	84.6	451	2	US-09-920-171-16	Sequence 16, Appli
28	2030	84.6	451	2	US-09-716-028-14	Sequence 14, Appli
29	2030	84.6	451	2	US-09-716-028-16	Sequence 16, Appli
30	2030	84.6	451	2	US-10-113-996-14	Sequence 14, Appli
31	2030	84.6	451	2	US-10-113-996-16	Sequence 16, Appli
32	2030	84.6	451	2	US-09-925-179-65	Sequence 65, Appli
33	2029.5	84.6	449	2	US-09-679-397-2	Sequence 2, Appli
34	2029.5	84.6	449	2	US-09-680-148-2	Sequence 2, Appli
35	2029.5	84.6	449	2	US-09-304-465A-2	Sequence 2, Appli
36	2029.5	84.6	449	2	US-10-356-974-2	Sequence 71, Appli
37	2029.5	84.6	452	2	US-09-027-449-71	Sequence 71, Appli
38	2029.5	84.6	452	2	US-09-026-985-71	Sequence 71, Appli
39	2029.5	84.6	452	2	US-09-121-952A-71	Sequence 71, Appli
40	2029.5	84.6	452	2	US-09-234-340A-71	Sequence 71, Appli
41	2029.5	84.6	452	2	US-09-355-014-71	Sequence 71, Appli
42	2029.5	84.6	452	3	US-09-726-258-71	Sequence 71, Appli
43	2029	84.6	470	2	US-10-020-786-9	Sequence 9, Appli
44	2027.5	84.5	467	2	US-08-523-89A-10	Sequence 10, Appli
45	2023	84.3	451	2	US-09-925-179-68	Sequence 68, Appli

ALIGNMENTS

RESULT 1

PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai:
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 443
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-13152-4

Query Match 91.2%; Score 2189; DB 5; Length 443;
Best Local Similarity 92.0%; Pred. No. 8.7e-161;

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Cv protein - protein search, using sw model

Run on: June 6, 2006, 04:47:35 ; Search time 26.9954 Seconds
(without alignments)
1607.447 Million cell updates/sec

Title: US-10-724-274-31

Perfect score: 2399

Sequence: 1 EVOLVSGGLVQPGGSLRL.....MHEALHNHYTKSLSLGK 451

Summary table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scored: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR_80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1743	72.7	327	1 G4HU	Ig gamma-4 chain C
2	1605.5	66.9	326	1 G2HU	Ig gamma-2 chain C
3	1590.5	66.3	330	1 GHU	Ig gamma-1 chain C
4	1585	66.1	377	2 A60764	Ig gamma-3 chain C
5	1575	65.7	377	2 A3511	Ig gamma-3 chain C
6	1524	63.5	470	2 S22080	Ig heavy chain pre
7	1479	61.7	472	2 S31459	Ig gamma-1 chain -
8	1466.5	61.1	444	2 PC4436	monoclonal antibod
9	1436.5	59.9	469	2 S37483	Ig gamma-2a chain
10	1431	59.6	446	2 S40295	Ig gamma-2a chain
11	1373	57.2	374	2 S63339	Ig heavy chain v
12	1344	56.0	474	1 G2MS11	Ig gamma-2b chain
13	1324.5	55.2	475	2 S01321	Ig gamma-2b chain
14	1289.5	53.8	328	2 I47159	Ig gamma 2a chain
15	1283.5	53.5	328	2 I47160	Ig gamma 2b chain
16	1264.5	52.7	328	2 I47161	Ig gamma 3 chain c
17	1240.5	51.7	328	2 I47158	Ig gamma 1 chain c
18	1199	50.0	323	1 GHRB	Ig gamma chain C r
19	1162	48.4	329	1 G2GP	Ig gamma-2 chain C
20	1147	47.8	308	2 C30554	Ig heavy chain C r
21	1139.5	47.5	255	4 S31866	Ig gamma-1 chain C
22	1129.5	47.1	234	2 P20207	Ig gamma chain C r
23	1124	46.9	333	2 PS0018	Ig gamma-2b chain
24	1118.5	46.6	326	2 PS0017	Ig gamma-1 chain C
25	1108.5	46.2	289	1 G3HUW1	Ig gamma-3 heavy c
26	1108	46.2	329	2 S00847	Ig gamma-2c chain
27	1106.5	46.1	324	1 G1MS	Ig gamma-1 chain C
28	1106.5	46.1	330	1 G2MSA	Ig gamma-2a chain
29	1103	46.0	327	2 S06611	Ig gamma-2 chain C

ALIGNMENTS

RESULT 1

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004

C:Accession: A90933; A90249; A02150

R:Elison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <ELL>

A:Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190

A:Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30;81-326 <PIN>

A:Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1, 111/1, 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,141-201,247-305/Disulfide bonds: #status predicted

F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Aen)

Query Match 72.7%; Score 1743; DB 1; Length 327;

Best Local Similarity 100.0%; Pred. No. 8.8e-94; Indels 0; Gaps 0;

Matches 327; Conservative 0; Mismatches 0;

QY 125 ASTKPSVFPPLAPCSRSTSEALGCLVKDYFPBPVTVMNSGALTSGVHTFPAVLQSS 184

Db 1 ASTKPSVFPPLAPCSRSTSEALGCLVKDYFPBPVTVMNSGALTSGVHTFPAVLQSS 60

QY 185 GLYSLSVVVTFPSSSLGTNTYTCNVDPKPSNTKVDKRVESKYGPPCPAPFELGGPSV 244

Db 61 GLYSLSVVVTFPSSSLGTNTYTCNVDPKPSNTKVDKRVESKYGPPCPAPFELGGPSV 120

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C: protein - protein search, using sw model

R: on: June 6, 2006, 04:37:25 ; Search time 208.628 Seconds
(without alignments)

1999.647 Million cell updates/sec

le: US-10-724-274-31

fect score: 2399

uence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHHYTKQSLSLGK 451

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 2849598 seqs, 925015592 residues

al number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

D: abase: Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

R: ult No.	Score	Query Match	Length	DB	ID	Description
1	2041.5	85.1	469	2	Q569F4_HUMAN	Q569F4 homo sapien
2	2029	84.6	472	2	Q6N089_HUMAN	Q6N089 homo sapien
3	2022	84.3	478	2	Q6P181_HUMAN	Q6P181 homo sapien
4	2020	84.2	464	2	Q6M2U6_HUMAN	Q6M2U6 homo sapien
5	2016	84.0	470	2	Q6PJA4_HUMAN	Q6PJA4 homo sapien
6	2012.5	83.9	465	2	Q6P6C4_HUMAN	Q6P6C4 homo sapien
7	2009	83.7	473	2	Q6TC83_HUMAN	Q6TC83 homo sapien
8	2008	83.7	466	2	Q6IN78_HUMAN	Q6IN78 homo sapien
9	2003.5	83.5	473	2	Q6M2V7_HUMAN	Q6M2V7 homo sapien
10	2002.5	83.5	476	2	Q6M2X7_HUMAN	Q6M2X7 homo sapien
11	1987	82.8	470	2	Q7Z5W1_HUMAN	Q7Z5W1 homo sapien
12	1985.5	82.8	544	2	Q6PJ95_HUMAN	Q6PJ95 homo sapien
13	1983	82.7	466	2	Q6N096_HUMAN	Q6N096 homo sapien
14	1979.5	82.5	475	2	Q6GMW7_HUMAN	Q6GMW7 homo sapien
15	1974.5	82.3	475	2	Q5EF85_HUMAN	Q5EF85 homo sapien
16	1971.5	82.2	475	2	Q6M2O6_HUMAN	Q6M2O6 homo sapien
17	1963	81.8	480	2	Q6N094_HUMAN	Q6N094 homo sapien
18	1954	81.5	470	2	Q68CNA_HUMAN	Q68CNA homo sapien
19	1942.5	81.0	473	2	Q6P055_HUMAN	Q6P055 homo sapien
20	1937.5	80.8	521	2	Q6N4Y9_HUMAN	Q6N4Y9 homo sapien
21	1934	80.6	482	2	Q7Z351_HUMAN	Q7Z351 homo sapien
22	1923.5	80.2	481	2	Q6N097_HUMAN	Q6N097 homo sapien
23	1921	80.1	476	2	Q6GMX1_HUMAN	Q6GMX1 homo sapien
24	1918.5	80.0	465	2	Q6GMX6_HUMAN	Q6GMX6 homo sapien
25	1900.5	79.2	475	2	Q6N095_HUMAN	Q6N095 homo sapien
26	1898	78.9	518	2	Q6N030_HUMAN	Q6N030 homo sapien
27	1893	78.7	417	2	Q6N093_HUMAN	Q6N093 homo sapien
28	1887.5	78.4	519	2	Q5EBM2_HUMAN	Q5EBM2 homo sapien
29	1882	78.4	480	2	Q6PJF1_HUMAN	Q6PJF1 homo sapien
30	1872.5	78.1	475	2	Q5RE17_PONPY	Q5RE17 pongo pygma
31	1869.5	77.9	469	2	Q7Z7P5_HUMAN	Q7Z7P5 homo sapien

32 1743 72.7 327 1 IGHG4_HUMAN P01861 homo sapien
33 1669 69.6 348 2 Q6PVX1_HUMAN Q6PVX1 homo sapien
34 1605.5 66.9 326 1 IGHG2_HUMAN P01859 homo sapien
35 1590.5 66.3 330 1 IGHG1_HUMAN P01857 homo sapien
36 1571 65.5 509 2 Q8NF17_HUMAN Q8NF17 homo sapien
37 1551.5 64.7 467 2 Q4VBH1_RAT Q4VBH1 rattus norv
38 1533.5 63.9 469 2 Q5M839_RAT Q5M839 rattus norv
39 1519.5 63.3 465 2 Q510J0_RAT Q510J0 rattus norv
40 1508 62.9 468 2 Q569B4_RAT Q569B4 rattus norv
41 1506 62.8 470 2 Q4G060_RAT Q4G060 rattus norv
42 1492 62.2 458 2 Q5M842_RAT Q5M842 rattus norv
43 1486.5 62.0 461 2 Q5M7V3_RAT Q5M7V3 rattus norv
44 1472 61.4 458 2 Q652Q1_HUMAN Q652Q1 homo sapien
45 1470 61.3 354 2 Q86TT2_HUMAN Q86TT2 homo sapien

ALIGNMENTS

RESULT 1
Q569F4_HUMAN PRELIMINARY; PRT; 469 AA.

AC Q569F4;

DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.

DT 10-MAY-2005, sequence version 1.

DT 07-FEB-2006, entry version 8.

DE IGHG1 protein.

GN Name=IGHG1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Buthera; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lymph;

RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RC TISSUE=Lymph;

RG NIH WGC Project;

RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.

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EMBL; BC092518; AA92518.1; --; mRNA.

DR SMR; Q569F4; 20-469.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.